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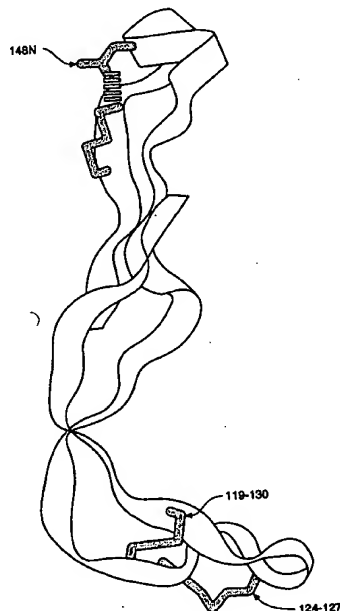
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(54) Title: MUTANT α -AMYLASE HAVING INTRODUCED THEREIN A DISULFIDE BOND

(57) Abstract

Novel α -amylase enzymes are disclosed in which one or more disulfide bonds are introduced into the enzyme via addition or substitution of a residue with a cysteine. The disclosed α -amylase enzymes show altered or improved stability and/or activity profiles.



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MUTANT α -AMYLASE
HAVING INTRODUCED THEREIN A DISULFIDE BOND

FIELD OF THE INVENTION

5 The present invention is directed to mutant α -amylases having introduced therein one or more disulfide bonds. In particular, the disulfide bonds are introduced by mutation of a precursor α -amylase to introduce one or more cysteine residues so as to produce a disulfide bond between two cysteine residues in said mutant α -amylase. It is specifically contemplated that the mutant will have altered performance characteristics such as altered stability and/or altered activity profiles.

10 BACKGROUND OF THE INVENTION

α -Amylases (α -1,4-glucan-4-glucanohydrolase, EC 3.2.1.1) hydrolyze internal α -1,4-glucosidic linkages in starch, largely at random, to produce smaller molecular weight malto-dextrins. α -Amylases are of considerable commercial value, being used in the initial stages (liquefaction) of starch processing; in alcohol production; as cleaning agents in detergent matrices; 15 and in the textile industry for starch desizing. α -Amylases are produced by a wide variety of microorganisms including *Bacillus* and *Aspergillus*, with most commercial amylases being produced from bacterial sources such as *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, or *Bacillus stearothermophilus*. In recent years, the preferred enzymes in commercial use 20 have been those from *Bacillus licheniformis* because of their heat stability and performance under commercial operating conditions.

In general, starch to fructose processing consists of four steps: liquefaction of granular starch, saccharification of the liquefied starch into dextrose, purification, and isomerization to fructose. The object of a starch liquefaction process is to convert a concentrated suspension of starch polymer granules into a solution of soluble shorter chain length dextrins of low viscosity. 25 This step is essential for convenient handling with standard equipment and for efficient conversion to glucose or other sugars. To liquefy granular starch, it is necessary to gelatinize the granules by raising the temperature of the granular starch to over about 72°C. The heating process instantaneously disrupts the insoluble starch granules to produce a water soluble starch solution. 30 The solubilized starch solution is then liquefied by α -amylase (EC 3.2.1.1.).

A common enzymatic liquefaction process involves adjusting the pH of a granular starch slurry to between 6.0 and 6.5, the pH optimum of α -amylase derived from *Bacillus licheniformis*, with the addition of calcium hydroxide, sodium hydroxide or sodium carbonate. The addition of calcium hydroxide has the advantage of also providing calcium ions which are known to stabilize the α - 35 amylases against inactivation. Upon addition of α -amylases, the suspension is pumped through a steam jet to instantaneously raise the temperature to between 80-115°C. The starch is immediately

gelatinized and, due to the presence of α -amylases, depolymerized through random hydrolysis of a(1-4) glycosidic bonds to a fluid mass which is easily pumped.

In a second variation to the liquefaction process, α -amylase is added to the starch suspension, the suspension is held at a temperature of 80-100°C to partially hydrolyze the starch granules, and the partially hydrolyzed starch suspension is pumped through a jet at temperatures in excess of about 105°C to thoroughly gelatinize any remaining granular structure. After cooling the gelatinized starch, a second addition of α -amylase can be made to further hydrolyze the starch.

A third variation of this process is called the dry milling process. In dry milling, whole grain is ground and combined with water. The germ is optionally removed by flotation separation or equivalent techniques. The resulting mixture, which contains starch, fiber, protein and other components of the grain, is liquefied using α -amylase. The general practice in the art is to undertake enzymatic liquefaction at a lower temperature when using the dry milling process. Generally, low temperature liquefaction is believed to be less efficient than high temperature liquefaction in converting starch to soluble dextrins.

Typically, after gelatinization the starch solution is held at an elevated temperature in the presence of α -amylase until a DE of 10-20 is achieved, usually a period of 1-3 hours. Dextrose equivalent (DE) is the industry standard for measuring the concentration of total reducing sugars, calculated as D-glucose on a dry weight basis. Unhydrolyzed granular starch has a DE of virtually zero, whereas the DE of D-glucose is defined as 100.

The maximum temperature at which the starch solution containing α -amylase can be held depends upon the microbial source from which the enzyme was obtained and the molecular structure of the α -amylase molecule. α -Amylases produced by wild type strains of *Bacillus subtilis* or *Bacillus amyloliquefaciens* are typically used at temperatures no greater than about 90°C due to excessively rapid thermal inactivation above that temperature, whereas α -amylases produced by wild type strains of *Bacillus licheniformis* can be used at temperatures up to about 110°C. The presence of starch and calcium ion are known to stabilize α -amylases against inactivation. Nonetheless, α -amylases are used at pH values above 6 to protect against rapid inactivation. At low temperatures, α -amylase from *Bacillus licheniformis* is known to display hydrolyzing activity on starch substrate at pH values as low as 5. However, when the enzyme is used for starch hydrolysis at common jet temperatures, e.g., between 102°C and 109°C, the pH must be maintained above at least pH 5.7 to avoid excessively rapid inactivation. The pH requirement unfortunately provides a narrow window of processing opportunity because pH values above 6.0 result in undesirable by-products, e.g., maltulose. Therefore, in reality, liquefaction pH is generally maintained between 5.9 and 6.0 to attain a satisfactory yield of hydrolyzed starch.

Another problem relating to pH of liquefaction is the need to raise the pH of the starch suspension from about 4, the pH of a corn starch suspension as it comes from the wet milling stage, to 5.9-6.0. This pH adjustment requires the costly addition of acid neutralizing chemicals

and also requires additional ion-exchange refining of the final starch conversion product to remove the chemical. Moreover, the next process step after liquefaction, typically saccharification of the liquefied starch into glucose with glucoamylase, requires a pH of 4-4.5; therefore, the pH must be adjusted back down from 5.9-6.0 to 4-4.5; requiring additional chemical addition and refining steps.

Subsequent to liquefaction, the processed starch is saccharified to glucose with glucoamylase. A problem with present processes occurs when residual starch is present in the saccharification mixture due to an incomplete liquefaction of the starch, e.g., inefficient amylose hydrolysis by amylase. Residual starch is highly resistant to glucoamylase hydrolysis. It represents a yield loss and interferes with downstream filtration of the syrups.

Additionally, many α -amylases are known to require the addition of calcium ion for stability. This further increases the cost of liquefaction.

In U.S. Patent No. 5,322,778, liquefaction between pH 4.0 and 6.0 was achieved by adding an antioxidant such as bisulfite or a salt thereof, ascorbic acid or a salt thereof, erythorbic acid, or phenolic antioxidants such as butylated hydroxyanisole, butylated hydroxytoluene, or α -tocopherol to the liquefaction slurry. According to this patent, sodium bisulfite must be added in a concentration of greater than 5mM.

In U.S. Patent No. 5,180,669, liquefaction between a pH of 5.0 to 6.0 was achieved by the addition of carbonate ion in excess of the amount needed to buffer the solution to the ground starch slurry. Due to an increased pH effect which occurs with addition of carbonate ion, the slurry is generally neutralized by adding a source of hydrogen ion, for example, an inorganic acid such as hydrochloric acid or sulfuric acid.

In PCT Publication No. WO 95/35382, a mutant α -amylase is described having improved oxidation stability and having changes at positions 104, 128, 187 and/or 188 in *B. licheniformis* α -amylase.

In PCT Publication No. WO 96/23873, mutant α -amylases are described which have any of a number of mutations.

In PCT Publication No. WO 94/02597, a mutant α -amylase having improved oxidative stability is described wherein one or more methionines are replaced by any amino acid except cysteine or methionine.

In PCT publication No. WO 94/18314, a mutant α -amylase having improved oxidative stability is described wherein one or more of the methionine, tryptophan, cysteine, histidine or tyrosine residues is replaced with a non-oxidizable amino acid.

In PCT Publication No. WO 91/00353, the performance characteristics and problems associated with liquefaction with wild type *Bacillus licheniformis* α -amylase are approached by genetically engineering the α -amylase to include the specific substitutions Ala-111-Thr, His-133-Tyr and/or Thr-149-Ile.

Studies using recombinant DNA techniques to explore which residues are important for the catalytic activity of amylases and/or to explore the effect of modifying certain amino acids within the active site of various amylases and glycosylases have been conducted by various researchers (Vihinen et al., J. Biochem., Vol. 107, pp. 267-272 (1990); Holm et al., Protein Engineering, Vol. 3, pp. 181-191 (1990); Takase et al., Biochemica et Biophysica Acta, Vol. 1120, pp. 281-288 (1992); Matsui et al., FEBS Letters, Vol. 310, pp. 216-218 (1992); Matsui et al., Biochemistry, Vol. 33, pp. 451-458 (1992); Sogaard et al., J. Biol. Chem., Vol. 268, pp. 22480-22484 (1993); Sogaard et al., Carbohydrate Polymers, Vol. 21, pp. 137-146 (1993); Svensson, Plant Mol. Biol., Vol. 25, pp. 141-157 (1994); Svensson et al., J. Biotech. Vol. 29, pp. 1-37 (1993)). Researchers have also studied which residues are important for thermal stability (Suzuki et al., J. Biol. Chem., Vol. 264, pp. 18933-18938 (1989); Watanabe et al., Eur. J. Biochem. Vol. 226, pp. 277-283 (1994)); and one group has used such methods to introduce mutations at various histidine residues in a *Bacillus licheniformis* amylase, the rationale being that *Bacillus licheniformis* amylase which is known to be relatively thermostable when compared to other similar *Bacillus* amylases, has an excess of histidines and, therefore, it was suggested that replacing a histidine could affect the thermostability of the enzyme. This work resulted in the identification of stabilizing mutations at the histidine residue at the +133 position and the alanine residue at position +209 (Declerck et al., J. Biol. Chem., Vol. 265, pp. 15481-15488 (1990); FR 2 665 178-A1; Joyet et al., Bio/Technology, Vol. 10, pp. 1579-1583 (1992)).

The introduction of di-sulphide bonds into proteins by site-directed mutagenesis affords a means of stabilizing native, folded conformations, see e.g., Villafranca et al., Science, Vol. 222, pp. 782-788 (1983). Hazes et al., Prot. Eng., Vol. 2, No. 2, pp. 119-125 (1988) suggest introducing disulfide bonds to a protein via a modeling algorithm which starts with the generation of the C β position from the N, C α and C atom positions available from a known three-dimensional model. A first set of residues is selected on the basis of the C β -C β distances; the S γ positions are generated which satisfy the requirement that, with ideal values for the C α -C β and C β -S γ bond lengths and for the bond angle at C β , the distance between the S γ of residue 1 and C β of residue 2 in a pair (determined by the bond angle at S γ 2) is at, or very close to, its ideal value; and the two acceptable S γ positions are found for each cysteine and the four different conformations for each disulfide bond established. Finally the four conformations are subjected to energy minimization procedure to remove large deviations from ideal geometry and their final energies calculated. Sowdhamini et al., Prot. Eng., Vol. 3, No. 2, pp. 95-103 (1989) discloses that the introduction of disulfide bonds into proteins by site directed mutagenesis affords a means of stabilizing native folded conformations and suggests computer modeling techniques for assessing the stereochemical suitability of pairs of residues in proteins as potential sites for introduction of cysteine disulfide crosslinks. The authors suggest that the elemental condition for considering residue positions in proteins, as potential sites for cysteine introduction, to generate unstrained disulfides is that the

alpha carbon distance between the two cysteine residues to be joined via the disulfide bond ($C\alpha-C\alpha$) be less than or equal to 6.5 Angstroms and that the beta carbon distance between the two cysteine residues to be joined via the disulfide bond ($C\beta-C\beta$) distance of less than or equal to 4.5 Angstroms.

5 Despite the advances made in the prior art, a need exists for an α -amylase which is more effective in commercial liquefaction processes but which allows activity at lower pH than currently practical. Additionally, a need exists for improved amylases having characteristics which makes them more effective under the conditions of detergent use. Because commercially available amylases are not acceptable under many conditions due to stability problems, for example, the
10 high alkalinity and oxidant (bleach) levels associated with detergents, or temperatures under which they operate, there is a need for an amylase having altered, and preferably increased, performance profiles under such conditions.

SUMMARY OF THE INVENTION

15 It is an object of the present invention to provide an α -amylase having altered performance profiles.

 It is a further object of the present invention to provide an α -amylase having improved stability at high temperature.

 Accordingly, the present invention provides a mutant α -amylase having introduced therein
20 one or more cysteine residues, wherein at least one of the introduced cysteine residues is capable of forming a disulfide bond with another cysteine residue. Preferably, the introduced cysteine(s) and the other cysteine residue with which it is to form a disulfide bond correspond to positions in the precursor α -amylase having a $C\alpha-C\alpha$ bond distance of between about 4.4-6.8 Angstroms and a $C\beta-C\beta$ bond distance of between about 3.45 and 4.5 Angstroms. In a particularly preferred
25 embodiment of the invention, the α -amylase is derived from a bacterial or a fungal source and comprises a substitution corresponding to E119C/S130C and/or D124C/R127C *Bacillus licheniformis*. Most preferably, the α -amylase is derived from *Bacillus*.

 The invention further comprises nucleic acids encoding such mutant amylases, vectors comprising such nucleic acids, host cells transformed with such vectors and methods of
30 expressing mutant α -amylases utilizing such host cells.

 The invention further comprises the use of the mutant α -amylases according to the invention to liquefy starch in the starch processing pathway to glucose or other starch derivatives, as an additive in detergents such as laundry and dishwashing detergents, as a baking aid and for desizing of textiles.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates the regions of secondary structure which are stabilized by the introduction of E119C/S130C and D124C/R127C corresponding to *Bacillus licheniformis* α -amylase.

Figure 2 illustrates the DNA sequence of the gene for α -amylase from *Bacillus licheniformis* (NCIB 8061) (SEQ ID NO:1) and deduced amino acid sequence of the translation product (SEQ ID NO:2) as described by Gray et al., *J. Bacteriology*, Vol. 166, pp. 635-643 (1986).

Figure 3 illustrates the amino acid sequence (SEQ ID NO:3) of the mature α -amylase enzyme from *Bacillus licheniformis*.

Figure 4 illustrates an alignment of the primary structures of three *Bacillus* α -amylases. The *Bacillus licheniformis* α -amylase (Am-Lich) (SEQ ID NO:4) is described by Gray et al., *J. Bacteriology*, Vol. 166, pp. 635-643 (1986); the *Bacillus amyloliquefaciens* α -amylase (Am-Amylo) (SEQ ID NO:5) is described by Takkinen et al., *J. Biol. Chem.*, Vol. 258, pp. 1007-1013 (1983); and the *Bacillus stearothermophilus* α -amylase (Am-Stearo) (SEQ ID NO:6) is described by Ihara et al., *J. Biochem.*, Vol. 98, pp. 95-103 (1985).

Figure 5 illustrates plasmid pHP13 wherein Cm^R refers to chloramphenicol resistance, Em^R refers to erythromycin resistance and Rep pTA1060 refers to the origin of replication from plasmid pTA1060.

Figure 6 illustrates the pBLapr plasmid wherein BL AA refers to *Bacillus licheniformis* α -amylase gene; *aprE* refers to the promoter and signal peptide encoding region of the *aprE* gene; Amp^R refers to the ampicillin resistant gene from pBR322; and CAT refers to the chloramphenicol resistance gene from pC194.

Figure 7 illustrates the pHP.BL plasmid carrying the gene for *Bacillus licheniformis* α -amylase.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

" α -Amylase" means an enzymatic activity which cleaves or hydrolyzes the α (1-4)glycosidic bond, e.g., that in starch, amylopectin or amylose polymers. α -Amylase as used herein includes naturally occurring α -amylases as well as recombinant α -amylases. Preferred α -amylases in the present invention are those derived from *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*, as well as fungal α -amylases such as those derived from *Aspergillus* (i.e., *A. oryzae* and *A. niger*).

"Recombinant α -amylase" means an α -amylase in which the DNA sequence encoding the naturally occurring α -amylase is modified to produce a mutant DNA sequence which encodes the substitution, insertion or deletion of one or more amino acids in the α -amylase sequence compared to the naturally occurring α -amylase.

"Expression vector" means a DNA construct comprising a DNA sequence which is operably linked to a suitable control sequence capable of effecting the expression of said DNA in a suitable host. Such control sequences may include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome-binding sites, and sequences which control termination of transcription and translation. A preferred promoter is the *Bacillus subtilis aprE* promoter. The vector may be a plasmid, a phage particle, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the present specification, plasmid and vector are sometimes used interchangeably as the plasmid is the most commonly used form of vector at present. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which are, or become, known in the art.

"Host strain" or "host cell" means a suitable host for an expression vector comprising DNA encoding the α -amylase according to the present invention. Host cells useful in the present invention are generally procaryotic or eucaryotic hosts, including any transformable microorganism in which the expression of α -amylase according to the present invention can be achieved. Specifically, host strains of the same species or genus from which the α -amylase is derived are suitable, such as a *Bacillus* strain. Preferably, an α -amylase negative *Bacillus* strain (genes deleted) and/or an α -amylase and protease deleted *Bacillus* strain ($\Delta amyE$, Δapr , Δnpr) is used. Host cells are transformed or transfected with vectors constructed using recombinant DNA techniques. Such transformed host cells are capable of either replicating vectors encoding the α -amylase and its variants (mutants) or expressing the desired α -amylase.

"Liquefaction" or "liquefy" means a process by which starch is converted to shorter chain and less viscous dextrins. Generally, this process involves gelatinization of starch simultaneously with or followed by the addition of α -amylase.

According to the present invention, a mutant α -amylase is provided that has introduced therein a first cysteine residue which is capable of forming a disulfide bond with a second cysteine residue. Preferably, the first cysteine residue comprises an addition or a substitution to a precursor α -amylase. It is further possible to incorporate the second cysteine residue as an addition or substitution as well, and this may be preferable should a useful cysteine residue not be present in a location useful to stabilize the desired portion of the molecule. With respect to *Bacillus licheniformis* α -amylase, it is necessary to incorporate two cysteine residues as the wild type molecule possesses no cysteines. Addition or substitution of an amino acid as used herein refers to any modification of the amino acid sequence itself of the precursor α -amylase, but preferably refers to using genetic engineering to mutate a nucleic acid encoding the precursor α -amylase so as to encode the substituted or added cysteine residue in the expressed protein. The precursor α -amylases include naturally occurring α -amylases and recombinant α -amylases. Modification of the

precursor DNA sequence which encodes the amino acid sequence of the precursor α -amylase can be by methods described herein and in commonly owned U.S. Patent Nos. 4,760,025 and 5,185,258, incorporated herein by reference.

Also provided is a nucleic acid molecule (DNA) which encodes an amino acid sequence comprising the mutant α -amylase provided by the present invention, expression systems incorporating such DNA including vectors and phages, host cells transformed with such DNA, and anti-sense strands of DNA corresponding to the DNA molecule which encodes the amino acid sequence. Similarly, the present invention includes a method for producing a mutant α -amylase by expressing the DNA incorporated on an expression system which has been transformed into a host cell. The mutant α -amylase of the invention may be used in liquefaction of starch, as an ingredient in laundry detergents, automatic dishwashing detergents, hard surface cleaning products, in food processing including baking applications, in textile processing including as a desize agent, or in any other application in which α -amylase activity is useful.

The precursor α -amylase is produced by any source capable of producing α -amylase. Suitable sources of α -amylases are prokaryotic or eukaryotic organisms, including fungi, bacteria, plants or animals. Preferably, the precursor α -amylase is produced by a *Bacillus*; more preferably, by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*; most preferably, the precursor α -amylase is derived from *Bacillus licheniformis*.

Homologies have been found between almost all endo-amylases sequenced to date, ranging from plants, mammals, and bacteria (Nakajima et al., Appl. Microbiol. Biotechnol., Vol. 23, pp. 355-360 (1986); Rogers, Biochem. Biophys. Res. Commun., Vol. 128, pp. 470-476 (1985); Janecek, Eur. J. Biochem., Vol. 224, pp. 519-524 (1994)). There are four areas of particularly high homology in certain *Bacillus* amylases, as shown in Figure 4, wherein the underlined sections designate the areas of high homology. Sequence alignments have also been used to map the relationship between *Bacillus* endo-amylases (Feng et al., J. Molec. Evol., Vol. 35, pp. 351-360 (1987)). The relative sequence homology between *Bacillus stearothermophilus* and *Bacillus licheniformis* amylase is about 66% and that between *Bacillus licheniformis* and *Bacillus amyloliquefaciens* amylases is about 81%, as determined by Holm et al., Protein Engineering, Vol. 3, No. 3, pp. 181-191 (1990). While sequence homology is important, it is generally recognized that structural homology is also important in comparing amylases or other enzymes. For example, structural homology between fungal amylases and bacterial amylase has been suggested and, therefore, fungal amylases are encompassed within the present invention.

Among others, substitutions at residues corresponding to E119C/S130C and/or D124C/R127C in *Bacillus licheniformis* α -amylase are identified herein for substitution. Thus, specific residues such as E119 refer to an amino acid position number (i.e., +119) which references the number assigned to the mature *Bacillus licheniformis* α -amylase sequence illustrated in Figure 2. The invention, however, is not limited to the mutation of the particular

mature α -amylase of *Bacillus licheniformis* but extends to precursor α -amylases containing amino acid residues at positions which are equivalent to the particular identified residue in *Bacillus licheniformis* α -amylase. A residue of a precursor α -amylase is equivalent to a residue of *Bacillus licheniformis* α -amylase if it is either homologous (i.e., corresponds in position for either the primary or tertiary structure) or analogous to a specific residue or portion of that residue in *Bacillus licheniformis* α -amylase (i.e., having the same or similar functional capacity to combine, react, or interact chemically or structurally).

In order to establish homology to primary structure, the amino acid sequence of a precursor α -amylase is directly compared to the *Bacillus licheniformis* α -amylase primary sequence and particularly to a set of residues known to be invariant to all α -amylases for which sequences are known (see e.g., Figure 4). It is possible also to determine equivalent residues by tertiary structure analysis of the crystal structures reported for porcine pancreatic α -amylase (Buisson et al., EMBO Journal, Vol. 6, pp. 3909-3916 (1987); Qian et al., Biochemistry, Vol. 33, pp. 6284-6294 (1994); Larson et al., J. Mol. Biol., Vol. 235, pp. 1560-1584 (1994)); Taka-amylase A from *Aspergillus oryzae* (Matsuura et al., J. Biochem. (Tokyo), Vol. 95, pp. 697-702 (1984)); and an acid α -amylase from *A. niger* (Boel et al., Biochemistry, Vol. 29, pp. 6244-6249 (1990)), with the former two structures being similar, and for barley α -amylase (Vallee et al., J. Mol. Biol., Vol. 236, pp. 368-371 (1994); Kadziola, J. Mol. Biol., Vol. 239, pp. 104-121 (1994)). Several preliminary studies have been published related to the secondary structure of α -amylase, i.e., (Suzuki et al., J. Biochem., Vol. 108, pp. 379-381 (1990); Lee et al., Arch. Biochem. Biophys., Vol. 291, pp. 255-257 (1991); Chang et al., J. Mol. Biol., Vol. 229, pp. 235-238 (1993); Mizuno et al., J. Mol. Biol., Vol. 234, pp. 1282-1283 (1993)), and at least one structure has been published for crystalline *Bacillus licheniformis* α -amylase (Machius et al., J. Mol. Biol. Vol. 246, pp. 545-549 (1995)). However, several researchers have predicted common super-secondary structures between glucanases (MacGregor et al., Biochem. J., Vol. 259, pp. 145-152 (1989)) and within α -amylases and other starch-metabolising enzymes (Jaspersen, J. Prot. Chem. Vol. 12, pp. 791-805 (1993); MacGregor, Starke, Vol. 45, pp. 232-237 (1993)); and sequence similarities between enzymes with similar super-secondary structures to α -amylases (Janecek, FEBS Letters, Vol. 316, pp. 23-26 (1993); Janecek et al., J. Prot. Chem., Vol. 12, pp. 509-514 (1993)). A structure for the *Bacillus stearothermophilus* enzyme has been modeled on that of Taka-amylase A (Holm et al., Protein Engineering, Vol. 3, pp. 181-191 (1990)). The four highly conserved regions shown in Figure 4 contain many residues thought to be part of the active-site (Matsuura et al., J. Biochem. (Tokyo), Vol. 95, pp. 697-702 (1984); Buisson et al., EMBO Journal, Vol. 6, pp. 3909-3916 (1987); Vihinen et al., J. Biochem., Vol. 107, pp. 267-272 (1990)) including His +105; Arg +229; Asp +231; His +235; Glu +261 and Asp +328 under the *Bacillus licheniformis* numbering system.

In the practice of the present invention, certain parameters are useful to determine with specificity appropriate substitutions. Information regarding the crystal structure of a specific enzyme should be obtained. Crystal structures from *Bacillus licheniformis* α -amylase, pig pancreatic α -amylase, *Aspergillus niger* and *Aspergillus oryzae* α -amylase, and barley α -amylase indicated, supra, are useful for this purpose. With information related to the crystal structure of the target enzyme, it is then useful to obtain information related to the instability of the enzyme under specific conditions, and preferably to obtain information related to the presence of specific unstable residues or regions which contribute to overall instability of the enzyme. As a specific example, Applicants were aware that α -amylase derived from *Bacillus licheniformis* comprises several residues that are particularly unstable under oxidizing conditions, i.e., M197 and W138. In the practice of the present invention, Applicants specifically studied the region surrounding S148 due to the ability of the S148N mutation to confer increased stability. The hypothesis that this region may have secondary structure elements which are made more stable by this substitution led Applicants to attempt to stabilize the enzyme via introduction of disulfide bonds into the proximal regions of secondary structure.

To determine the specific residues for substitution, the distances between the alpha carbons and the beta carbons for each of the residues in the folded protein were measured from the crystal structure to determine which pairs fall within the allowable distances for a disulfide bond were both residues cysteines. For example, the residue pair for which it is contemplated to incorporate substitution(s) resulting in two cysteine residues should preferably have an alpha carbon distance ($C\alpha-C\alpha$) of between about 4.4 and about 6.8 Angstroms. Similarly, the beta carbon distance ($C\beta-C\beta$) should be between about 3.45 and 4.5 Angstroms. Selecting amino acid pairs which fall within these criteria for carbon distance and utilizing strategies outlined in Swodhamini et al., supra, and Hazes et al., supra, it was possible to minimize the disturbance of the protein which may be caused by the substitution of a cysteine and the subsequent formation of a disulfide bond between two such cysteines. In this way, it is possible to select a first and second cysteine residue for which conditions are favorable for the formation of a disulfide bond. Applicants thus singled out D124-R127 and E119-S130 as particularly preferred substitutions. However, any residue pair may be utilized so long as it falls within the appropriate criteria provided herein.

α -Amylases according to the present invention which exhibit altered performance characteristics providing desirable and unexpected results are useful in the various applications for which α -amylases are commonly used. For example, α -amylases according to the present invention which exhibit altered performance characteristics at low pH, including improved thermostability, improved pH stability and/or improved oxidative stability, are useful in low pH liquefaction of starch. Enhanced thermostability will be useful in extending the shelf life of products which incorporate them. Enhanced oxidative stability or improved performance is

particularly desirable in cleaning products, and for extending the shelf life of α -amylase in the presence of bleach, perborate, percarbonate or peracids used in such cleaning products. To the contrary, reduced thermal stability or oxidative stability may be useful in industrial processes which require the rapid and efficient quenching of amylolytic activity.

5 α -Amylases of the present invention which exhibit improved low pH stability will be especially useful in starch processing and particularly in starch liquefaction. Conditions present during commercially desirable liquefaction processes characteristically include low pH, high temperature and potential oxidation conditions requiring α -amylases exhibiting improved low pH performance, improved thermal stability and improved oxidative stability. Accordingly, α -amylases
10 according to the present invention which are particularly useful in liquefaction exhibit improved performance at a pH of less than about 6, preferably less than about 5.5, and most preferably less than about 5.0. Additionally, α -amylases according to the present invention which exhibit increased thermal stability at temperatures of between about 80-120°C, and preferably between about 100-110°C, and increased stability in the presence of oxidants will be particularly useful.

15 Additional components known by those skilled in the art to be useful in liquefaction, including, for example, antioxidants, calcium, ions, salts or other enzymes such as endoglycosidases, cellulases, proteases, lipases or other amylase enzymes may be added depending on the intended reaction conditions. For example, combinations of the α -amylase according to the present invention with α -amylases from other sources may provide unique action
20 profiles which find particular use under specific liquefaction conditions. In particular, it is contemplated that the combination of the α -amylase according to the present invention with α -amylase derived from *Bacillus stearothermophilus* will provide enhanced liquefaction at pH values below 5.5 due to complementary action patterns.

During liquefaction, starch, specifically granular starch slurries from either a wet or dry
25 milled process, is treated with an α -amylase of the present invention according to known liquefaction techniques. Generally, in the first step of the starch degradation process, the starch slurry is gelatinized by heating at a relatively high temperature (between about 80°C and about 110°C). After the starch slurry is gelatinized, it is liquefied using an α -amylase.

In another embodiment of the present invention, detergent compositions in either liquid, gel
30 or granular form, which comprise the α -amylase according to the present invention may be useful. Such detergent compositions will particularly benefit from the addition of an α -amylase according to the present invention which has increased thermal stability to improve shelf-life or increased oxidative stability such that the α -amylase has improved resistance to bleach or peracid compounds commonly present in detergents. Thus, α -amylase according to the present invention
35 may be advantageously formulated into known powdered, liquid or gel detergents having a pH of between about 6.5 and about 12.0. Detergent compositions comprising the α -amylase according to the present invention may further include other enzymes such as endoglycosidases, cellulases,

proteases, lipases or other amylase enzymes, particularly α -amylase derived from *Bacillus stearothermophilus*, as well as additional ingredients as generally known in the art.

A preferred embodiment of the present invention further comprises, in addition to the substitution of two or more cysteine residues, any one or more of the substitutions known in the art to confer stability or increased activity. For example, the deletion or substitution of a methionine residue or a tryptophan residue, for example M15, M197 or W138 as described in WO 94/18314, the disclosure of which is incorporated herein by reference; substitution at H133Y as described in PCT Publication No. WO 91/00353; or substitution at A209 as described in DeClerck, et al., *J. Biol. Chem.*, Vol. 265, pp. 15481-15488 (1990); or any of the substitutions described in PCT Publication Nos.

WO 95/10603, WO 96/23873 and WO 96/23874. In particularly preferred embodiments, the α -amylase according to the present invention may further comprise a deletion or substitution at one or more residues corresponding to M15, A33, A52, S85, N96, V128, H133, S148N, S187, N188, A209, A269 and/or A379 in *Bacillus licheniformis* α -amylase. Particular embodiments of the amylase of the present invention may comprise a substitution pattern corresponding to M15T/E119C/S130C/N188S, M15L/E119C/S130C/N188S, M15T/E119C/S130C/H133Y/N188S, M15T/E119C/S130C/H133Y/N188S/A209V, M15T/E119C/S130C/N188S/A209V, M15T/E119C/V128E/S130C/H133Y/N188S, M15T/E119C/S130C/S187D/N188S, M15T/E119C/S130C/H133Y, M15T/E119C/S130C/H133Y/N188S/A209V, M15T/E119C/S130C/H133Y/A209V or, M15T/E119C/S130C/H133Y/S148N/A209V/A379S in *Bacillus licheniformis*.

Embodiments of the present invention which comprise a combination of the α -amylase according to the present invention with protease enzymes preferably include oxidatively stable proteases such as those described in U.S. Re. 34,606, incorporated herein by reference, as well as commercially available enzymes such as DURAZYM (Novo Nordisk) and PURAFECT® OXP (Genencor International, Inc.). Methods for making such protease mutants (oxidatively stable proteases), and particularly such mutants having a substitution for the methionine at a position equivalent to M222 in *Bacillus amyloliquefaciens*, are described in U.S. Re. 34,606.

An additional embodiment of the present invention comprises DNA encoding an α -amylase according to the present invention and expression vectors comprising such DNA. The DNA sequences may be expressed by operably linking them to an expression control sequence in an appropriate expression vector and employing that expression vector to transform an appropriate host according to well-known techniques. A wide variety of host/expression vector combinations may be employed in expressing the DNA sequences of this invention. Useful expression vectors, for example, include segments of chromosomal, non-chromosomal and synthetic DNA sequences, such as the various known plasmids and phages useful for this purpose. In addition, any of a wide variety of expression control sequences are generally used in these vectors. For example,

Applicants have discovered that a preferred expression control sequence for *Bacillus* transformants is the *aprE* signal peptide derived from *Bacillus subtilis*.

5 A wide variety of host cells are also useful in expressing the DNA sequences of this invention. These hosts may include well-known eukaryotic and prokaryotic hosts, such as strains of *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*, various fungi, yeast and animal cells. Preferably, the host expresses the α -amylase of the present invention extracellularly to facilitate purification and downstream processing. Expression and purification of the mutant α -amylase of the invention may be effected through art-recognized means for carrying out such processes.

10 The improved α -amylases according to the present invention are contemplated to provide several important advantages when compared to wild type *Bacillus* α -amylases. For example, one advantage is the increased activity found at low pH and high temperatures typical of common starch liquefaction methods. Another advantage is the increased high pH and oxidative stability which facilitates their use in detergents. Another advantage is that a more complete hydrolysis of starch molecules is achieved which reduces residual starch in the processing stream. Yet another
15 advantage is their improved stability in the absence of calcium ion. Yet another advantage is that the addition of equal protein doses of α -amylase according to the invention provide superior performance when compared to wild type *Bacillus licheniformis* α -amylase due to improvements in both specific activity and stability under stressed conditions. In other words, because of the generally increased stability of the amylases according to the present invention, the increased
20 specific activity on starch of the inventive amylases translates to even greater potential performance benefits of this variant. Under conditions where the wild type enzyme is being inactivated, not only does more of the inventive amylase survive because of its increased stability, but also that which does survive expresses proportionally more activity because of its increased specific activity.

25 The following is presented by way of example and is not to be construed as a limitation to the scope of the claims. Abbreviations used herein, particularly three letter or one letter notations for amino acids are described in Dale, J.W., Molecular Genetics of Bacteria, John Wiley & Sons, (1989) Appendix B.

EXAMPLES

30

EXAMPLE 1

Construction Of Plasmid pHP.BL

35 The α -amylase gene shown in Figure 2 was cloned from *Bacillus licheniformis* NCIB8061 (Gray et al., J. Bacteriology, Vol. 166, pp. 635-643 (1986)). The 1.72kb PstI-SstI fragment, encoding the last three residues of the signal sequence, the entire mature protein and the terminator region, was subcloned into M13mp18. A synthetic terminator was added between the BclI and SstI sites using a synthetic oligonucleotide cassette of the form:

5'-GATCAAAACATAAAAAACCGGCCTTGGCCCCGCCGGTTTTTTATTATTTTGTAGCT-3' (SEQ ID NO:7)
 3'-TTTTGTATTTTGGCCGAACCGGGGCGCCAAAAAATAATAAAAC-5' (SEQ ID NO:8)

designed to contain the *Bacillus amyloliquefaciens* subtilisin transcriptional terminator (Wells et al.,

5 Nucleic Acid Research, Vol. 11, pp. 7911-7925 (1983)).

The pBLapr plasmid was constructed carrying the gene for the *Bacillus licheniformis* α -amylase. As illustrated in Figure 6, pBLapr comprises a 6.1kb plasmid including the ampicillin resistance gene from pBR322 and the chloramphenicol resistance gene from pC194, the aprE promoter and the gene encoding for the *Bacillus licheniformis* α -amylase ("BL AA"). The aprE promoter was constructed from a 660bp HindIII-PstI fragment encoding for the promoter and signal sequence of the *Bacillus subtilis* alkaline protease. The PstI site was removed, and an SfiI site added close to the aprE/BL AA junction. The BL AA gene comprises the 1720 bp PstI-SstI fragment described above. In the work described herein, pBLapr was constructed with an SfiI site adjacent to the 5' end of the start of the coding sequence for the mature amylase gene.

15 Specifically, the 5' end of the pBLapr construction was subcloned on an EcoRI-SstII fragment from pBLapr into M13BM20 (Boehringer Mannheim) to obtain a coding-strand template for the mutagenic oligonucleotide below:

5'-CCC ATT AAG ATT GGC CGC CTG GGC CGA CAT GTT GCT GG - 3' (SEQ ID NO:9)

20

This primer introduced an SfiI site (indicated by underlining) which allowed correct forms to be screened for by the presence of this unique restriction site. Subcloning the EcoRI-SstII fragment back into the pBLapr vector gave a version of the plasmid containing an SfiI site.

Plasmid pHP13 (Haima et al., Mol. Gen. Genet., Vol. 209, pp. 335-342 (1987)) (Figure 5) was digested with restriction enzymes EcoRI and HindIII and the resulting vector purified on a polyacrylamide gel and then eluted. Plasmid pBLapr was digested with HindIII, Asp718 and in a separate incubation with Asp718, EcoRI and gel purified. Two bands, HindIII-Asp718 (1203 bp) and Asp718-EcoRI (1253 bp) were gel purified, eluted from the gel and ligated into the vector by a 3-way ligation, to give plasmid pHP.BL, the plasmid used in expression of the α -amylase (Figure 7).

30

EXAMPLE 2

Construction Of Plasmid Encoding α -Amylase Comprising Substitutions At E119C/S130C Or D124C/R127C

A pBLapr plasmid having threonine substituted for methionine at amino acid 15 was constructed according to U.S. Patent Application Serial No. 08/194,664 (PCT Publication No. WO 94/18314). To introduce the additional cysteine residues, the following mutagenic primers encoding for substitutions of E119C/S130C and D124C/R127C were used together with non-mutagenic primers to introduce the desired mutations into linear multiple tandem repeats of the plasmid by the method of multimerization as described below.

35

119C/130C

AA CCg Cgg TTT gCg TCg ATC CCg CTg ACC gCA ACC gCg TAA TTT gCg gAg AAC ACC (SEQ ID NO:10)

124C/127C

TCg ATC CCg CTT gCC gCA ACTgCg TAA TTT CAg gAg AA (SEQ ID NO:11)

A fragment starting at the mutagenic primer (shown above) and ending at the 3' end of the coding region was generated by PCR. This fragment was gel purified and used to generate long, linear tandem repeats of the plasmid encoding the desired cysteine mutations as follows:

The vector (pBLapr/M15T) was linearized by restriction digest (Sal I) and purified using Qiagen kits. The multimerization reactions typically contained 5.4 mM Tris buffer pH 8.0, 1x XL buffer (Perkin Elmer, Branchburg, NJ), 0.2 mM dNTPs, 1.1 mM Mg(OAc)₂, 3 ng/μl incoming fragment, 0.15 ng/μl linearized vector, 4 U *rTth* DNA polymerase, XL (Perkin Elmer) in 100 μl reaction mixture. PCR reactions were typically performed in a thermocycler under the following conditions: 20 cycles (15s 94°C, 5 min 68°C) and 15 cycles (15s 94°C, 10 min 68°C).

The resulting multimers were transformed directly into *B. subtilis* competent cells using standard techniques. Plasmid DNA was isolated from the transformants using standard techniques.

Mutations were confirmed by dideoxy sequencing (Sanger et al., Proc. Natl. Acad. Sci. U.S.A., Vol. 74, pp. 5463-5467 (1977)).

EXAMPLE 3Transformation Of Plasmids Into *Bacillus subtilis*,
Expression And Purification Of Mutant α-Amylase

α-Amylase may be expressed in *Bacillus subtilis* after transformation with the plasmids described above. pHP13 is a plasmid able to replicate in *E. coli* and in *Bacillus subtilis*. Plasmids containing different variants were constructed using *E. coli* strain MM294, the plasmids isolated and then transformed into *Bacillus subtilis* as described in Anagnostopoulos et al., J. Bacter., Vol. 81, pp. 741-746 (1961). The *Bacillus* strain had been deleted for two proteases (Δapr, Δnpr) (see e.g., Ferrari et al., U.S. Patent No. 5,264,366) and for amylase (ΔamyE) (see e.g., Stahl et al., J. Bacter., Vol. 158, pp. 411-418 (1984)). After transformation, the sacU(Hy) mutation (Henner et al., J. Bacter., Vol. 170, pp. 296-300 (1988)) was introduced by PBS-1 mediated transduction (Hoch, J. Bact., Vol. 154, pp. 1513-1515 (1983)).

Secreted amylase was recovered from *Bacillus subtilis* cultures as follows: Sodium chloride was added to the culture supernatant to 20mM and the pH was adjusted to approximately 7.0 with 1M tris buffer, pH 7.2. The supernatant was then heated to 70°C for 15 minutes, and the precipitate removed by centrifugation. Ammonium sulphate was added the supernatant to 1.3M followed by 20ml phenyl sepharose fast flow 6 (high substitution) resin (Pharmacia). Following agitation, resin was separated by filtration, and washed in 1M ammonium sulphate, 20mM

ammonium acetate pH 7.0, 5mM calcium chloride. The bound amylase was eluted into 20mM ammonium acetate pH 7.0, 5mM calcium chloride, and precipitated by addition of ammonium sulphate to 70% saturation. The precipitated material was pelleted by centrifugation, redissolved in a minimum volume of 20mM ammonium acetate pH 7.0, 5mM calcium chloride and dialysed against the same buffer.

Concentration was determined using the soluble substrate assay, assuming wild-type specific activity.

EXAMPLE 4

Assay For Determining α -Amylase Activity

Soluble Substrate Assay: A rate assay was developed based on an end-point assay kit supplied by Megazyme (Aust.) Pty. Ltd. A vial of substrate (*p*-nitrophenyl maltoheptaoside, BPNPG7) was dissolved in 10ml of sterile water followed by a 1:4 dilution in assay buffer (50mM maleate buffer, pH 6.7, 5mM calcium chloride, 0.002% Tween20). Assays were performed by adding 10 μ l of amylase to 790 μ l of the substrate in a cuvette at 25°C. Rates of hydrolysis were measured as the rate of change of absorbance at 410nm, after a delay of 75 seconds. The assay was linear up to rates of 0.2 absorption units/min.

α -Amylase protein concentration was measured using the standard Bio-Rad Assay (Bio-Rad Laboratories) based on the method of Bradford, Anal. Biochem., Vol. 72, p. 248 (1976) using bovine serum albumin standards.

EXAMPLE 5

Preparation and Testing of Additional Mutant Alpha-Amylases for Thermal Stability

Mutant *B. licheniformis* alpha-amylases were prepared having substitutions at M15T or M15T/E119C/S130C. Thermal inactivation rates for the various mutants were measured according to the following procedure. Amylase stock solutions were dialysed extensively into 20 mM ammonium acetate, 4 mM CaCl₂ pH 6.5. Each sample was split into two equal vials and dithiothreitol added to one of the vials at 10 mM and stored at least overnight at 4°C. For measurement of stability, this stock was diluted >50fold into 50mM ammonium acetate, 5mM CaCl₂, 0.02% Tween 20 pH 4.8 to a final concentration of between 30 and 50 μ g/ml. For those stocks containing 10mM DTT, the dilution buffers contained 1mM DTT. Six 100 μ l aliquots were put into eppendorf tubes and placed into a water bath or hot block at 83°C. The eppendorf tubes were removed at regular, measured intervals of between 30 seconds and 5 minutes and placed on ice to stop the inactivation. The residual activity was assayed using a soluble substrate as described in Example 4. The natural log of the activity was plotted against time of incubation, and the rate constant for inactivation obtained from the slope of the straight line. Results for various mutants are provided in Table 1.

TABLE 1

Amylase Mutant	Temperature	Inactivation Rate Constant $k(\text{min}^{-1})$	Half Life (minutes)
M15T/E119C/S1 30C (+DTT)	63.9	0.0278	24.932
M15T/E119C/S1 30C (+DTT)	65	0.0461	25.035
M15T/E119C/S1 30C (+DTT)	66.2	0.0632	10.967
M15T/E119C/S1 30C (+DTT)	67.4	0.0884	7.840
M15T/E119C/S1 30C (+DTT)	68.5	0.102	6.795
M15T/E119C/S1 30C (+DTT)	69.5	0.124	5.590
M15T/E119C/S1 30C (+DTT)	70.4	0.168	4.126
M15T/E119C/S1 30C (+DTT)	71.3	0.202	3.431
M15T/E119C/S1 30C (+DTT)	74.2	0.67	1.034
M15T/E119C/S1 30C (+DTT)	74.2	0.682	1.016
M15T/E119C/S1 30C (-DTT)	67.5	0.0481	14.410
M15T/E119C/S1 30C (-DTT)	69	0.0728	9.521
M15T/E119C/S1 30C (-DTT)	70.2	0.0978	7.087
M15T/E119C/S1 30C (-DTT)	71.4	0.145	4.780
M15T/E119C/S1 30C (-DTT)	72.5	0.186	3.726
M15T/E119C/S1 30C (-DTT)	73.4	0.254	2.729
M15T/E119C/S1 30C (-DTT)	74.5	0.305	2.272
M15T/E119C/S1 30C (-DTT)	75.5	0.4	1.733
M15T/E119C/S1 30C (-DTT)	72.9	0.158	4.387
M15T/E119C/S1 30C (-DTT)	72.9	0.156	4.443
M15T/E119C/S1 30C (-DTT)	72.9	0.146	4.747
M15T	67.5	0.051	13.590
M15T	69	0.082	8.452
M15T	70.2	0.112	6.188
M15T	71.4	0.143	4.847
M15T	72.5	0.191	3.629
M15T	72.9	0.199	3.483
M15T	72.9	0.208	3.332
M15T	72.9	0.244	2.841
M15T	73.4	0.208	3.332
M15T	74.5	0.302	2.295
M15T	75.5	0.421	1.646

As shown in Table 1, mutant enzymes having introduced therein two cysteine residues capable of forming a disulfide bond showed significantly increased stability over the mutant M15T

enzyme with no introduces cysteine bonds. Additionally, as shown in Table 1, mutant enzymes having introduced therein a disulfide bond between E119C and S130C showed significantly improved stability over the M15T mutant or the M15T/E119C/S130C mutant which was treated with DTT (i.e., disulfide bond reduced and/or broken).

WE CLAIM:

1. A mutant α -amylase capable of forming a disulfide bond between a first and a second cysteine residue, wherein said mutant α -amylase is derived from a precursor α -amylase and said first cysteine residue results from a substitution or addition of an amino acid to said precursor α -amylase.
2. The mutant α -amylase according to claim 1, wherein said first cysteine residue corresponds to a residue in said precursor α -amylase having a C α -C α bond distance of between about 4.4-6.8 Angstroms and a C β -C β bond distance of between about 3.45 and 4.5 Angstroms with said second cysteine residue or a residue corresponding to said second cysteine residue in said precursor α -amylase.
3. The α -amylase according to claim 2, wherein said α -amylase comprises a substitution corresponding to E119C/S130C and/or D124C/R127C *Bacillus licheniformis*.
4. The α -amylase according to claim 1, wherein said α -amylase is derived from a bacterial or fungal source.
5. The α -amylase according to claim 1, wherein said α -amylase is derived from *Bacillus*.
6. The α -amylase according to claim 5, wherein said α -amylase is derived from *Bacillus licheniformis*, *Bacillus stearothermophilus* or *Bacillus amyloliquefaciens*.
7. The α -amylase according to claim 1 wherein said α -amylase further comprises the deletion or substitution of a residue corresponding to M15, A33, A52, S85, N96, V129, H133, S148N, S187, N188, A209, A269 and/or A379 in *Bacillus licheniformis*.
8. An α -amylase that is the expression product of a mutated DNA sequence encoding an α -amylase, the mutated DNA sequence being derived from a precursor α -amylase by a substitution corresponding to M15T/E119C/S130C/N188S, M15L/E119C/S130C/N188S, M15T/E119C/S130C/H133Y/N188S, M15T/E119C/S130C/H133Y/N188S/A209V, M15T/E119C/S130C/N188S/A209V, M15T/E119C/N128E/S130C/H133Y/N188S, M15T/E119C/S130C/S187D/N188S, M15T/E119C/S130C/H133Y/N188S/A209V, M15T/E119C/S130C/H133Y/S148N/N188S/A209V/A379S, or M15T/E119C/S130C/H133Y in *Bacillus licheniformis*.

9. The α -amylase according to claim 1, wherein substitution further comprises substituting or deleting a residue corresponding to M15T, W138Y and/or M197T in *Bacillus licheniformis*.
10. A DNA encoding the α -amylase according to claim 1.
11. An expression vector comprising the DNA of claim 10.
12. A host cell transformed with the expression vector of claim 11.
13. An α -amylase according to claims 1, 3 or 7 having enhanced low pH performance.
14. A detergent composition comprising the α -amylase according to claim 1.
15. The detergent composition according to claim 14, wherein said detergent is useful for cleaning soiled laundry and/or soiled dishes.
16. A method of liquefying starch comprising contacting a slurry of starch with the α -amylase according to claim 1.

1 / 10

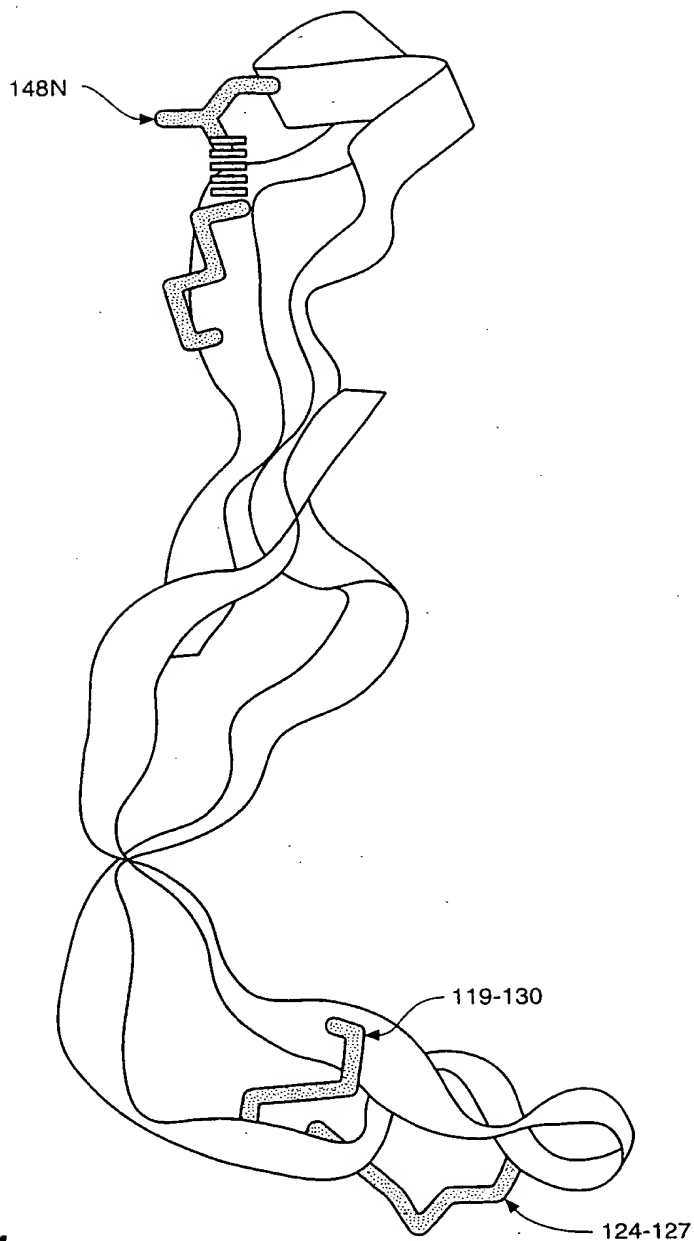


FIG._1

2 / 10

10 30 50
AGCTTGAAGAAGTGAAGAAGCAGAGAGGCTATTGAATAAATGAGTAGAAAGCGCCATATC

70 90 110
GGCGCTTTTCTTTTGAAGAAAATATAGGGAAAATGGTACTTGTTAAAAATTTCGGAATAT

130 150 170
TTATACAACATCATATGTTTCACATTGAAAGGGGAGGAGAATCATGAAACAACAAAAACG
M K Q Q K R

190 210 230
GCTTTACGCCCGATTGCTGACGCTGTTATTTGCGCTCATCTTCTTGCTGCCTCATTCTGC
L Y A R L L T L L F A L I F L L P H S A

250 270 290
AGCAGCGGCGGCAAAATCTTAATGGGACGCTGATGCAGTATTTGAATGGTACATGCCCAA
A A A A N L N G T L M Q Y F E W Y M P N

310 330 350
TGACGGCCAACATTGGAAGCGTTTGCAAAACGACTCGGCATATTTGGCTGAACACGGTAT
D G Q H W K R L Q N D S A Y L A E H G I

370 390 410
TACTGCCGTCTGGATTCCCCCGGCATATAAGGGAACGAGCCAAGCGGATGTGGGCTACGG
T A V W I P P A Y K G T S Q A D V G Y G

430 450 470
TGCTTACGACCTTTATGATTTAGGGGAGTTTCATCAAAAAGGGACGGTTCGGACAAAGTA
A Y D L Y D L G E F H Q K G T V R T K Y

490 510 530
CGGCACAAAAGGAGAGCTGCAATCTGCGATCAAAAGTCTTCATTCCCGCGACATTAACGT
G T K G E L Q S A I K S L H S R D I N V

550 570 590
TTACGGGGATGTGGTCATCAACCACAAAGGCGGCGCTGATGCGACCGAAGATGTAACCGC
Y G D V V I N H K G G A D A T E D V T A

610 630 650
GGTTGAAGTCGATCCCGCTGACCGCAACCGCGTAATTTCAAGGAGAACACCTAATTAAGC
V E V D P A D R N R V I S G E H L I K A

670 690 710
CTGGACACATTTTCATTTTCCGGGGCGCGGCAGCACATACAGCGATTTTAAATGGCATTG
W T H F H F P G R G S T Y S D F K W H W

730 750 770
GTACCATTTTGACGGAACCGATTGGGACGAGTCCCGAAAAGCTGAACCGCATCTATAAGTT
Y H F D G T D W D E S R K L N R I Y K F

790 810 830
TCAAGGAAAGGCTTGGGATTGGGAAGTTTCCAATGAAAACGGCAACTATGATTATTTGAT
Q G K A W D W E V S N E N G N Y D Y L M

FIG. 2A

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850 870 890
GTATGCCGACATCGATTATGACCATCCTGATGTGCGCAGCAGAAATTAAGAGATGGGGCAC
Y A D I D Y D H P D V A A E I K R W G T

910 930 950
TTGGTATGCCAATGAACTGCAATTGGACGGTTTCCGTCTTGATGCTGTCAAACACATTAA
W Y A N E L Q L D G F R L D A V K H I K

970 990 1010
ATTTTCTTTTTGCGGGATTGGGTTAATCATGTGAGGGAAAAACGGGGAAGGAAATGTT
F S F L R D W V N H V R E K T G K E M F

1030 1050 1070
TACGGTAGCTGAATATTGGCAGAATGACTTGGGCGCGCTGGAAAACATTTGAACAAAAC
T V A E Y W Q N D L G A L E N Y L N K T

1090 1110 1130
AAATTTTAATCATTCACTGTTTGACGTGCCGCTTCATTATCAGTTCATGCTGCATCGAC
N F N H S V F D V P L H Y Q F H A A S T

1150 1170 1190
ACAGGGAGGCGGCTATGATATGAGGAAATTGCTGAACGGTACGGTCTTTCCAAGCATCC
Q G G G Y D M R K L L N G T V V S K H P

1210 1230 1250
GTTGAAATCGGTTACATTTGTCGATAACCATGATACACAGCCGGGGCAATCGCTTGAGTC
L K S V T F V D N H D T Q P G Q S L E S

1270 1290 1310
GACTGTCCAAACATGGTTTAAGCCGCTTGCTTACGCTTTTATTCTCACAAGGGAATCTGG
T V Q T W F K P L A Y A F I L T R E S G

1330 1350 1370
ATACCCCTCAGGTTTTCTACGGGGATATGTACGGGACGAAAGGAGACTCCCAGCGCGAAAT
Y P Q V F Y G D M Y G T K G D S Q R E I

1390 1410 1430
TCCTGCCTTGAAACACAAAATTGAACCGATCTTAAAAGCGAGAAAACAGTATGCGTACGG
P A L K H K I E P I L K A R K Q Y A Y G

1450 1470 1490
AGCACAGCATGATTATTTGACCAACCATGACATTGTCGGCTGGACAAGGGAAGCGACAG
A Q H D Y F D H H D I V G W T R E G D S

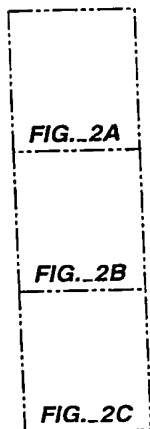
1510 1530 1550
CTCGTTGCAAATTCAGGTTTGGCGGCATTAATAACAGACGGACCCGTTGGGGCAAAGCG
S V A N S G L A A L I T D G P G G A K R

1570 1590 1610
AATGTATGTCGGCCGGCAAAAACGCCGGTGAGACATGGCATGACATTACCGGAAACCGTTC
M Y V G R Q N A G E T W H D I T G N R S

1630 1650 1670
GGAGCCGGTTGTCATCAATTCGGAAGGCTGGGGAGAGTTTCACGTAAACGGCGGGTCCGT
E P V V I N S E G W G E F H V N G G S V

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1690 1710 1730
TTCAATTTATGTTCAAAGATAGAAGAGCAGAGAGGACGGATTTCTGAAGGAAATCCGTT
S I Y V Q R *
1750 1770 1790
TTTTTATTTTGCCCGTCTTATAAATTTCTTTGATTACATTTTATAATTAATTTTAACAAA
1810 1830 1850
GTGTCATCAGCCCTCAGGAAGGACTTGCTGACAGTTTGAATCGCATAGGTAAGCGGGGA
1870 1890 1910
TGAAATGGCAACGTTATCTGATGTAGCAAAGAAAGCAAATGTGTGAAAATGACGGTATC
1930 1950
GCGGGTGATCAATCATCCTGAGACTGTGACGGATGAATTGAAAAAGCT

FIG._2C**FIG._2**

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10 30 50
ANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLA EHGITAVWIPPAYKGT SQADVGYGAYD

70 90 110
LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKG GADATEDVTAVEV

130 150 170
DPADRN RVISGEHLIKAWTHFHFPGRGSTY SDFKWHWYHFDGTDWDES RKLNR IYKFQ GK

190 210 230
AWDWEVSNENGN YDYL MYADIDYDHPDVA AEIKRWGTWYAN ELQLDGFRLDAVKHIKFSF

250 270 290
LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNH SVFDVPLHYQFHAAS TQGG

310 330 350
GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGY PQ

370 390 410
VFYGD MYGT KGDSQREIPALKHKIEPILKARKQYAYGAQH DYFDHHDIVGW TREGDSSVA

430 450 470
NSGLAALITDGP GGAKRMYVGRQNAGETWHDITGNRSEPVVINSEG WGEFHVNGG SVSIY

VQR

FIG. 3

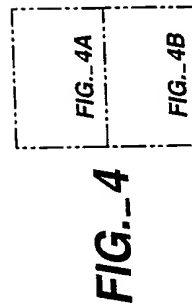
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Am-Lich = <i>B. Licheniformis</i>	Am-Amylo = <i>B. amyloliquefaciens</i>	Am-Stearo = <i>B. stearothermophilus</i>	
1	1	1	
Am-Lich	Am-Amylo	Am-Stearo	19
Am-Amylo	Am-Amylo	Am-Stearo	60
Am-Stearo	Am-Amylo	Am-Stearo	79
61	61	61	120
Am-Lich	Am-Amylo	Am-Stearo	139
Am-Amylo	Am-Amylo	Am-Stearo	180
Am-Stearo	Am-Amylo	Am-Stearo	197
121	121	121	240
Am-Lich	Am-Amylo	Am-Stearo	257
Am-Amylo	Am-Amylo	Am-Stearo	300
Am-Stearo	Am-Amylo	Am-Stearo	317
181	181	181	360
Am-Lich	Am-Amylo	Am-Stearo	
Am-Amylo	Am-Amylo	Am-Stearo	
Am-Stearo	Am-Amylo	Am-Stearo	
241	241	241	
Am-Lich	Am-Amylo	Am-Stearo	
Am-Amylo	Am-Amylo	Am-Stearo	
Am-Stearo	Am-Amylo	Am-Stearo	
301	301	301	
Am-Lich	Am-Amylo	Am-Stearo	
Am-Amylo	Am-Amylo	Am-Stearo	
Am-Stearo	Am-Amylo	Am-Stearo	

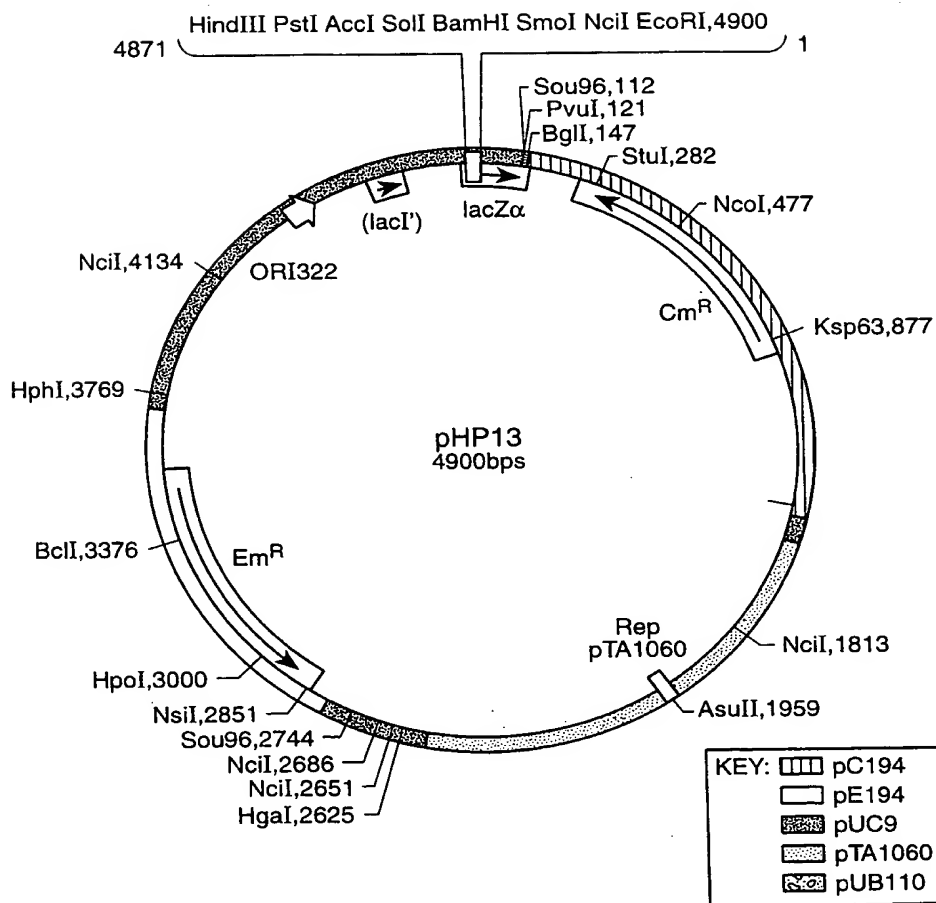
FIG. 4A

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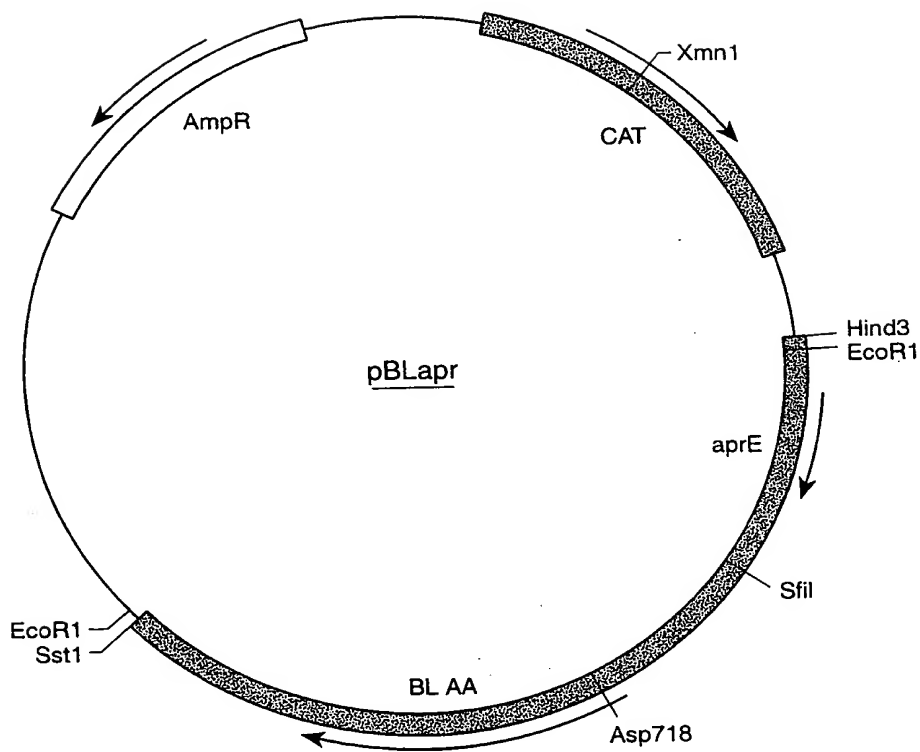
361	Am-Lich	LKSVTFVDNH	DTQPGQSLES	TVQTWFKPLA	YAFILTRESG	YPQVFYGDY	GTKGDSQREI	377
	Am-Amylo	EKAFTFVENH	DTQPGQSLES	TVQTWFKPLA	YAFILTRESG	YPQVFYGDY	GTKGTSPKEI	420
	Am-Stearo	TLAVTFVDNH	DTNPAKR..CS	HGRPWFKPLA	YAFILTRQEG	YPCVFYGDY	GI.....PQYNI	437
421	Am-Lich	PALKHKIEPI	LKARKQYAYG	AQHDYFDHHD	IVGWTREGDS	SVANSGLAAL	ITDGPGGAKR	480
	Am-Amylo	PSLKDNIIEPI	LKARKEYAYG	PQHDYIDHPD	VIGWTREGDS	SAAKSGLAAL	ITDGPGGSKR	
	Am-Stearo	PSLKSISKIDPL	LIARRDYAYG	TQHDYLDHSD	IIGWTREGVT	EKPGSGLAAL	ITDGAGRSKW	
481	Am-Lich	MYVGRQNAGE	TWHDITGNRS	EPVVINSEGW	GEFHVNGGSV	SIYVQR.....		540
	Am-Amylo	MYAGLKNAGE	TWYDITGNRS	DTVKIGSDGW	GEFHVNDGSV	SIYVQK.....		
	Am-Stearo	MYVGKQHAGK	VFYDLTGNRS	DTVTINSDBG	GEFKVNGGSV	SVWVPRKTTV	STIARPIITR	
541	Am-Lich	
	Am-Amylo	
	Am-Stearo	PWTGEFVRWH	EPRLVAWP*	

FIG.--4B**FIG.--4**

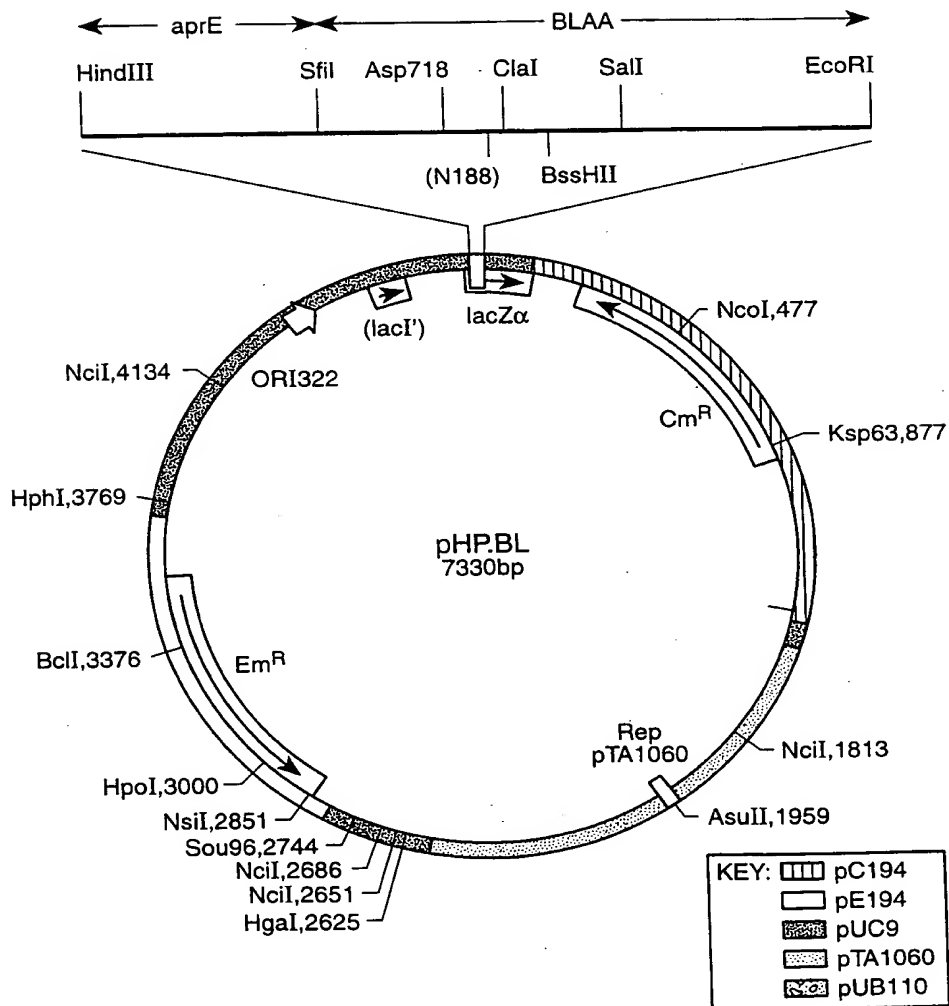
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**FIG._5**

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**FIG. 6**

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**FIG. 7**

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/13572

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/55 C12N9/28 C12P19/14 C12S3/12 C11D3/386
C12N1/21 //(C12N9/28,C12R1:10)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C12P C11D C12S

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SOWDHAMINI R ET AL: "Stereochemical modeling of disulfide bridges. Criteria for introduction into proteins by site-directed mutagenesis." PROTEIN ENGINEERING, vol. 3, no. 2, 1989, pages 95-103, XP002085412 cited in the application see abstract see table VI see page 96, column 1, line 4 - page 97, column 1, line 23</p> <p style="text-align: center;">--- -/--</p>	1,2

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

Date of mailing of the international search report

23 November 1998

08/12/1998

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Authorized officer

Lejeune, R

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/13572

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MANSFELD J ET AL: "EXTREME STABILIZATION OF A THERMOLYSIN-LIKE PROTEASE BY AN ENGINEERED DISULFIDE BOND" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 272, no. 17, 25 April 1997, pages 11152-11156, XP002074322 see abstract ---	1,2
A	WO 96 39528 A (GENENCOR INT ;MITCHINSON COLIN (GB); REQUADT CAROL (US); ROPP TRAC) 12 December 1996 see claims ---	7-9
A	WO 96 30481 A (GENENCOR INT) 3 October 1996 see claims ---	7-9
A	WO 95 35382 A (GIST BROCADES BV ;LAAN JAN METSKE V D (NL); AEHLE WOLFGANG (NL)) 28 December 1995 cited in the application see claims 1-4 ---	7,8
A	FR 2 665 178 A (AGRONOMIQUE INST NAT RECH) 31 January 1992 cited in the application see abstract ---	7,8
A	WO 95 10603 A (BORCHERT TORBEN VEDEL ;THELLERSEN MARIANNE (DK); ZEE PIA V D (DK);) 20 April 1995 cited in the application see claim 17 -----	7,8

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Information on patent family members

International Application No

PCT/US 98/13572

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